

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YYNSSSVYSFGEGLPTCFWFILQIPEHRRIMLSPEVVQALLVEELLSTVNSSAAMPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGGQGVRLRKGPDLHASSCLWHLQGGPKDMLM
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFAQEVNLTLDNRLDSQGVLPSTPYFPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTCQCGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCGEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEHCD
CGLQGPPSSRIVGGAVSSEGEWFWQASLQVRGRHICGGALIAIRWVITAAHCFQEDSMASITVL
WTVFLGKVMQNSRWPGVESFKVSRLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSAYRYQVTPRMLCAGYRKG
KKDACQGDGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

05978205-101504

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TAGCCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCGTGTGCGGGTGCCTATGGCTTGTACAACAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTTCGTGAATGGAATCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCTGGATGAGAGAACTGCGTTTGACAGGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACTTCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGGCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGATTTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTGCGGGTGCACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCAGGAGGACAGCAT
GGCCTCCACGGTGTGTGTGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGTCTCTGCACCCGTACCAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACACCCGGTGGTGCCTCGGCCCGCTGCGCCC
CGTCTGCCTGCCCGCGCTGCCACTTCTTCGAGCCCGCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGATGTGCAAGTTG
ATCCCAAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGACTCAGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGTTCTTGGCGGGGCTGGTCACTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGCTACACCCGATCACAGGTGTGATCAGTGGATCCAGCAAGTGGT
GACCTGAGGAAGTGCCTCCCTGCAAGAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGACAAGTAT

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAACACCAAGAGGTGGTTTTTGTTTTTTAAA
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGTACCTCTCCGTGCGGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTTGAAAATCGCTGCACAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGAAGATGCAGATTTTG
TGGATGTCTCCACACCTACACGCGTTCTTTCGGCTTGAGCATTGGTATTAGATGCGCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTCCTTCCAGTGCAT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTCAGAGGTAACTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACTCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAAATCGTTGCAAAATCAGATTACACTGTGCATGTCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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